Appl. No. 10/650,559
Reply to Office Action of 7/15/2009

Attorney Docket No: U2002-0057US01

AMENDMENTS TO THE SPECIFICATION

Please replace page 8 of the Specification with the following replacement page:

modifications known in the art, both naturally occurring and non-naturally occurring.

      The terms "complementary" or "complement thereof" are used herein to refer to the sequences of polynucleotides which is capable of forming Watson & Crick base pairing with another specified polynucleotide throughout the entirety of the complementary region. For the purpose of the present disclosure, a first polynucleotide is deemed to be complementary to a second polynucleotide when each base in the first polynucleotide is paired with its complementary base. Complementary bases are, generally, A and T (or A and U), or C and G. "Complement" is used herein as a synonym from "complementary polynucleotide", "complementary nucleic acid" and "complementary nucleotide sequence".

      As used in this disclosure, the term "percent homology" of two amino acid sequences or of two nucleic acid sequences is determined using the algorithm of Karlin and Altschul (Karlin and Altschul, 1990. Proc. Natl. Acad. Sci. USA 87:22264-2268) modified as in Karlin and Altschul (Karlin and Altschul, 1993. Proc. Natl. Acad. Sci. USA 90:5873-5877). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (Altschul, et al., 1990. J. Mol. Biol. 215:403-410). Blast nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. Blast protein searches are performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a referenced polypeptide. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Altschul, et al. Nucleic Acids Res. 25:3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (XBLAST and NBLAST) are used. See http://www.ncbi.nlm.nih.gov.

      The term "functional derivatives" includes "fragments," "degenerate variants," "mutants," "variants," and "chemical derivatives." When referring to a polypeptide, the term "fragment" is meant to refer to any polypeptide subset of GBS phage lysin having the amino acid sequence shown in SEQ ID NO:2. In one embodiment, the fragment is at least 5 amino acids in length; however, the